Remarks

I. The Amendments

The specification of the application was amended to add sequence identification numbers. Attached hereto as an Appendix is a marked-up version of the text showing the changes that were made. It can be seen that, except for the sequence identification numbers, the original text has not been altered.

II. Submission of Computer Readable Form of Sequence Listing

Enclosed herewith is a 3.5 inch computer diskette containing a copy of the enclosed Sequence Listing in ASCII text.

III. Statements to Comply With Sequence Listing Rules

In compliance with 37 C.F.R. § 1.821(f), Applicants' undersigned attorney hereby states the content of the paper and computer readable copies of the Sequence Listing submitted herewith are the same. In accordance with 37 C.F.R. § 1.821(g), Applicants' undersigned attorney hereby states that the Sequence Listing submitted herewith does not add new matter to the application.

Conclusion

In light of the amendments and remarks above, Applicants submit that they have now fully complied with all Sequence Listing rules. It is therefore respectfully submitted that this application is now in condition for substantive review. If, in the opinion of the Examiner, a phone call may help to expedite the prosecution of this application, the Examiner is invited to call Applicants' undersigned attorney at (703) 905-2173.

Respectfully submitted,
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Appendix

Version with Markings to Show Changes Made

The specification has been amended herein to add sequence identification numbers. The changes that were made are shown below with the underlined words indicating text that was added.

On page 16, lines 5-34 to read as follows:

> In order to clone the insertion site located upstream of the transposon Tn5531 in the mutant described in Example 1.1, the chromosomal DNA of this mutant strain was first of all isolated as described by Schwarzer et al. (Bio/Technology (1990) 9: 84-87) and 400 ng of the latter was cut with the restriction endonuclease EcoRI. The complete restriction insert was ligated with the vector pUC18 likewise linearised with EcoRI (Norander et al., Gene (1983) 26: 101-106) from Roche Diagnostics (Mannheim, Germany). The E. coli strain DH5αmcr (Grant et al., Proceedings of the National Academy of Sciences of the United States of America USA (1990) 87: 4645-4649) was transformed with the complete ligation insert by means of electroporation (Dower et al., Nucleic Acid Research (1988) 16: 6127-6145). Transformants in which the insertion sites of the transposon Tn5531 were present cloned on the vector pUC18 were identified by means of their carbenicillin resistance and kanamycin resistance on LB-agar plates containing 50 µg/mL of carbenicillin and 25 µg/mL of kanamycin. The plasmids were prepared from three of the transformants and the sizes of the cloned inserts were determined by restriction analysis. The nucleotide sequence of the insertion site on one of the plasmids was determined with a ca. 5.7 kb large insert by the dideoxy chain termination method of Sanger et al. (Proceedings of the National Academy of Sciences of the United States of America USA (1977) 74: 5463-5467). For this purpose 2.2 kb of the insert were sequenced starting from the following oligonucleotide primer: 5'-CGG GTC TAC ACC GCT AGC CCA GG-3'. <u>(SEQ ID NO:5)</u>

On page 16 line 35 to page 17 line 11, to read as follows:

> In order to identify the insertion site located downstream of the transposon, the chromosomal DNA of the mutant was cut with the restriction endonuclease XbaI and ligated in the vector pUC18 linearised with XbaI. The further cloning was carried out as described above. The nucleotide sequence of the insertion site on one of the plasmids was determined with a ca. 8.5 kb large insert by the dideoxy chain termination method of Sanger et al. (Proceedings of the National Academy of Sciences of the United States of America USA

(1977) 74: 5463-5467). For this purpose 0.65 kb of the insert was sequenced starting from the following oligonucleotide primer: 5'-CGG TGC CTT ATC CAT TCA GG-3'. (SEQ ID NO:6)

On page 17, lines 30-33 to read as follows:

ThrE-forward:
5'-CCC CTT TGA CCT GGT GTT ATT G-3' (SEQ ID NO:7)
thrE-reverse:
5'-CGG CTG CGG TTT CCT CTT-3' (SEQ ID NO:8)

On page 18, lines 35-36 to read as follows:

Universal primer:
5'-GTA AAA CGA CGG CCA GT-3' (SEQ ID NO:9)

On page 19, lines 1-2 to read as follows:

Reverse primer:
5'-GGA AAC AGC (SEQ ID NO:10)